Basi ● ● 1600

┌───┐
│ This Raw Listing contains the General Information   │   *all*
│ Section and up to first 5 pages.   │   *P.5*
└───┘
                                                        ENTERED

```
 1    <110> APPLICANT: BOYD, Andrew W
 2           DOTTORI, Mirella
 3           LACKMANN, Martin
 4    <120> TITLE OF INVENTION: RECEPTOR-LIGAND SYSTEM AND ASSAY
 5    <130> FILE REFERENCE: boyduq
 6    <140> CURRENT APPLICATION NUMBER: US/09/104,340
 7    <141> CURRENT FILING DATE: 1998-06-25
 8    <150> EARLIER APPLICATION NUMBER: PO7549
 9    <151> EARLIER FILING DATE: 1997-06-25
10    <160> NUMBER OF SEQ ID NOS: 25
11    <170> SOFTWARE: PatentIn Ver. 2.0
12    <210> SEQ ID NO 1
13    <211> LENGTH: 220
14    <212> TYPE: PRT
15    <213> ORGANISM: Homo sapiens
16    <220> FEATURE:
17    <221> NAME/KEY: DOMAIN
18    <222> LOCATION: (1)..(220)
19    <223> OTHER INFORMATION: Encoded by Exon III of HEK gene
20    <400> SEQUENCE: 1
21          Trp Glu Glu Ile Ser Gly Val Asp Glu His Tyr Thr Pro Ile Arg Thr
22           1               5                  10                  15
23          Tyr Gln Val Cys Asn Val Met Asp His Ser Gln Asn Asn Trp Leu Arg
24                       20                  25                  30
25          Thr Asn Trp Val Pro Arg Asn Ser Ala Gln Lys Ile Tyr Val Glu Leu
26                       35                  40                  45
27          Lys Phe Thr Leu Arg Asp Cys Asn Ser Ile Pro Leu Val Leu Gly Thr
28                   50                  55                  60
29          Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Met Glu Ser Asp Asp His
30           65                  70                  75                  80
31          Gly Val Lys Phe Arg Glu His Gln Phe Thr Lys Ile Asp Thr Ile Ala
32                           85                  90                  95
33          Ala Asp Glu Ser Phe Thr Gln Met Asp Leu Gly Asp Arg Ile Leu Lys
34                       100                 105                 110
35          Leu Asn Thr Glu Ile Arg Glu Val Gly Pro Val Asn Lys Lys Gly Phe
36                       115                 120                 125
37          Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Val Ala Leu Val Ser Val
38                   130                 135                 140
39          Arg Val Tyr Phe Lys Lys Cys Pro Phe Thr Val Lys Asn Leu Ala Met
40           145                 150                 155                 160
41          Phe Pro Asp Thr Val Pro Met Asp Ser Gln Ser Leu Val Glu Val Arg
42                           165                 170                 175
43          Gly Ser Cys Val Asn Asn Ser Lys Glu Glu Asp Pro Pro Arg Met Tyr
44                       180                 185                 190
```

```
45        Cys Ser Thr Glu Gly Glu Trp Leu Val Pro Ile Gly Lys Cys Ser Cys
46                   195               200               205
47        Asn Ala Gly Tyr Glu Glu Arg Gly Phe Met Cys Gln
48                   210               215               220
49   <210> SEQ ID NO 2
50   <211> LENGTH: 22
51   <212> TYPE: PRT
52   <213> ORGANISM: Homo sapiens
53   <220> FEATURE:
54   <221> NAME/KEY: DOMAIN
55   <222> LOCATION: (1)..(22)
56   <223> OTHER INFORMATION: Encoded by Exon II of  HEK gene
57   <400> SEQUENCE: 2
58        Val Asn Leu Leu Asp Ser Lys Thr Ile Gln Gly Glu Leu Gly Trp Ile
59         1               5                   10                  15
60        Ser Tyr Pro Ser His Gly
61                     20
62   <210> SEQ ID NO 3
63   <211> LENGTH: 29
64   <212> TYPE: PRT
65   <213> ORGANISM: Homo sapiens
66   <220> FEATURE:
67   <221> NAME/KEY: DOMAIN
68   <222> LOCATION: (1)..(29)
69   <223> OTHER INFORMATION: Encoded by Exon I of HEK gene
70   <400> SEQUENCE: 3
71        Met Asp Cys Gln Leu Ser Ile Leu Leu Leu Leu Ser Cys Ser Val Leu
72         1               5                   10                  15
73        Asp Ser Phe Gly Glu Leu Ile Pro Gln Pro Ser Asn Glu
74                     20                  25
75   <210> SEQ ID NO 4
76   <211> LENGTH: 271
77   <212> TYPE: PRT
78   <213> ORGANISM: Homo sapiens
79   <400> SEQUENCE: 4
80        Met Asp Cys Gln Leu Ser Ile Leu Leu Leu Leu Ser Cys Ser Val Leu
81         1               5                   10                  15
82        Asp Ser Phe Gly Glu Leu Ile Pro Gln Pro Ser Asn Glu Val Asn Leu
83                     20                  25                  30
84        Leu Asp Ser Lys Thr Ile Gln Gly Glu Leu Gly Trp Ile Ser Tyr Pro
85                     35                  40                  45
86        Ser His Gly Trp Glu Glu Ile Ser Gly Val Asp Glu His Tyr Thr Pro
87                     50                  55                  60
88        Ile Arg Thr Tyr Gln Val Cys Asn Val Met Asp His Ser Gln Asn Asn
89             65                  70                  75                  80
90        Trp Leu Arg Thr Asn Trp Val Pro Arg Asn Ser Ala Gln Lys Ile Tyr
91                     85                  90                  95
92        Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Ile Pro Leu Val
93                     100                 105                 110
94        Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Met Glu Ser Asp
```

```
 95                    115                    120                    125
 96          Asp Asp His Gly Val Lys Phe Arg Glu His Gln Phe Thr Lys Ile Asp
 97              130                    135                    140
 98          Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Met Asp Leu Gly Asp Arg
 99              145                    150                    155                160
100          Ile Leu Lys Leu Asn Thr Glu Ile Arg Glu Val Gly Pro Val Asn Lys
101                             165                    170                    175
102          Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Val Ala Leu
103                             180                    185                    190
104          Val Ser Val Arg Val Tyr Phe Lys Lys Cys Pro Phe Thr Val Lys Asn
105                             195                    200                    205
106          Leu Ala Met Phe Pro Asp Thr Val Pro Met Asp Ser Gln Ser Leu Val
107              210                    215                    220
108          Glu Val Arg Gly Ser Cys Val Asn Asn Ser Lys Glu Glu Asp Pro Pro
109              225                    230                    235                240
110          Arg Met Tyr Cys Ser Thr Glu Gly Glu Trp Leu Val Pro Ile Gly Lys
111                             245                    250                    255
112          Cys Ser Cys Asn Ala Gly Tyr Glu Glu Arg Gly Phe Met Cys Gln
113                             260                    265                    270
114  <210> SEQ ID NO 5
115  <211> LENGTH: 813
116  <212> TYPE: DNA
117  <213> ORGANISM: Homo sapiens
118  <220> FEATURE:
119  <221> NAME/KEY: exon
120  <222> LOCATION: (1)..(813)
121  <223> OTHER INFORMATION: Exons I, II and III of HEK gene
122  <400> SEQUENCE: 5
123          atg gat tgt cag ctc tcc atc ctc ctc ctt ctc agc tgc tct gtt ctc      48
124          gac agc ttc ggg gaa ctg att ccg cag cct tcc aat gaa gtc aat cta      96
125          ctg gat tca aaa aca att caa ggg gag ctg ggc tgg atc tct tat cca     144
126          tca cat ggg tgg gaa gag atc agt ggt gtg gat gaa cat tac aca ccc     192
127          atc agg act tac cag gtg tgc aat gtc atg gac cac agt caa aac aat     240
128          tgg ctg aga aca aac tgg gtc ccc agg aac tca gct cag aag att tat     288
129          gtg gag ctc aag ttc act cta cga gac tgc aat agc att cca ttg gtt     336
130          tta gga act tgc aag gag aca ttc aac ctg tac tac atg gag tct gat     384
131          gat gat cat ggg gtg aaa ttt cga gag cat cag ttt aca aag att gac     432
132          acc att gca gct gat gaa agt ttc act caa atg gat ctt ggg gac cgt     480
133          att ctg aag ctc aac act gag att aga gaa gta ggt cct gtc aac aag     528
134          aag gga ttt tat ttg gca ttt caa gat gtt ggt gct tgt gtt gcc ttg     576
135          gtg tct gtg aga gta tac ttc aaa aag tgc cca ttt aca gtg aag aat     624
136          ctg gct atg ttt cca gac acg gta ccc atg gac tcc cag tcc ctg gtg     672
137          gag gtt aga ggg tct tgt gtc aac aat tct aag gag gaa gat cct cca     720
138          agg atg tac tgc agt aca gaa ggc gaa tgg ctt gta ccc att ggc aag     768
139          tgt tcc tgc aat gct ggc tat gaa gaa aga ggt ttt atg tgc caa         813
140  <210> SEQ ID NO 6
141  <211> LENGTH: 87
142  <212> TYPE: DNA
143  <213> ORGANISM: Homo sapiens
144  <220> FEATURE:
```

```
145    <221> NAME/KEY: exon
146    <222> LOCATION: (1)..(87)
147    <223> OTHER INFORMATION: Exon I of HEK gene
148    <400> SEQUENCE: 6
149         atg gat tgt cag ctc tcc atc ctc ctc ctt ctc agc tgc tct gtt ctc   48
150         gac agc ttc ggg gaa ctg att ccg cag cct tcc aat gaa               87
151    <210> SEQ ID NO 7
152    <211> LENGTH: 66
153    <212> TYPE: DNA
154    <213> ORGANISM: Homo sapiens
155    <220> FEATURE:
156    <221> NAME/KEY: exon
157    <222> LOCATION: (1)..(66)
158    <223> OTHER INFORMATION: Exon II of HEK gene
159    <400> SEQUENCE: 7
160         gtc aat cta ctg gat tca aaa aca att caa ggg gag ctg ggc tgg atc   48
161         tct tat cca tca cat ggg                                          66
162    <210> SEQ ID NO 8
163    <211> LENGTH: 660
164    <212> TYPE: DNA
165    <213> ORGANISM: Homo sapiens
166    <220> FEATURE:
167    <221> NAME/KEY: exon
168    <222> LOCATION: (1)..(660)
169    <223> OTHER INFORMATION: Exon III of HEK gene
170    <400> SEQUENCE: 8
171         tgg gaa gag atc agt ggt gtg gat gaa cat tac aca ccc atc agg act   48
172         tac cag gtg tgc aat gtc atg gac cac agt caa aac aat tgg ctg aga   96
173         aca aac tgg gtc ccc agg aac tca gct cag aag att tat gtg gag ctc   144
174         aag ttc act cta cga gac tgc aat agc att cca ttg gtt tta gga act   192
175         tgc aag gag aca ttc aac ctg tac tac atg gag tct gat gat gat cat   240
176         ggg gtg aaa ttt cga gag cat cag ttt aca aag att gac acc att gca   288
177         gct gat gaa agt ttc act caa atg gat ctt ggg gac cgt att ctg aag   336
178         ctc aac act gag att aga gaa gta ggt cct gtc aac aag aag gga ttt   384
179         tat ttg gca ttt caa gat gtt ggt gct tgt gtt gcc ttg gtg tct gtg   432
180         aga gta tac ttc aaa aag tgc cca ttt aca gtg aag aat ctg gct atg   480
181         ttt cca gac acg gta ccc atg gac tcc cag tcc ctg gtg gag gtt aga   528
182         ggg tct tgt gtc aac aat tct aag gag gaa gat cct cca agg atg tac   576
183         tgc agt aca gaa ggc gaa tgg ctt gta ccc att ggc aag tgt tcc tgc   624
184         aat gct ggc tat gaa gaa aga ggt ttt atg tgc caa               660
185    <210> SEQ ID NO 9
186    <211> LENGTH: 27
187    <212> TYPE: DNA
188    <213> ORGANISM: Artificial Sequence
189    <220> FEATURE:
190    <223> OTHER INFORMATION: Description of Artificial Sequence: HEK PCR primer
191    <400> SEQUENCE: 9
192         gtaggaattc ctctcactgc cctctgc                                    27
193    <210> SEQ ID NO 10
194    <211> LENGTH: 25
```

```
195     <212> TYPE: DNA
196     <213> ORGANISM: Artificial Sequence
197     <220> FEATURE:
198     <223> OTHER INFORMATION: Description of Artificial Sequence: HEK PCR primer
199     <400> SEQUENCE: 10
200          gtagggatcc ggcctcctgt tccag                              25
201     <210> SEQ ID NO 11
202     <211> LENGTH: 27
203     <212> TYPE: DNA
204     <213> ORGANISM: Artificial Sequence
205     <220> FEATURE:
206     <223> OTHER INFORMATION: Description of Artificial Sequence: HEK PCR primer
207     <400> SEQUENCE: 11
208          gtaggaattc catggcttgt acccgac                            27
209     <210> SEQ ID NO 12
210     <211> LENGTH: 27
211     <212> TYPE: DNA
212     <213> ORGANISM: Artificial Sequence
213     <220> FEATURE:
214     <223> OTHER INFORMATION: Description of Artificial Sequence: HEK PCR primer
215     <400> SEQUENCE: 12
216          gtagggatcc cataatgctt gcttctc                            27
217     <210> SEQ ID NO 13
218     <211> LENGTH: 20
219     <212> TYPE: DNA
220     <213> ORGANISM: Artificial Sequence
221     <220> FEATURE:
222     <223> OTHER INFORMATION: Description of Artificial Sequence: HEK PCR primer
223     <400> SEQUENCE: 13
224          atggatggta acttctccag                                    20
225     <210> SEQ ID NO 14
226     <211> LENGTH: 20
227     <212> TYPE: DNA
228     <213> ORGANISM: Artificial Sequence
229     <220> FEATURE:
230     <223> OTHER INFORMATION: Description of Artificial Sequence: HEK PCR primer
231     <400> SEQUENCE: 14
232          tcattggaag gctgcggaat                                    20
233     <210> SEQ ID NO 15
234     <211> LENGTH: 30
235     <212> TYPE: DNA
236     <213> ORGANISM: Artificial Sequence
237     <220> FEATURE:
238     <223> OTHER INFORMATION: Description of Artificial Sequence: HEK PCR primer
239     <400> SEQUENCE: 15
240          gtagtctaga caagcttgtc gaccaggttt                         30
241     <210> SEQ ID NO 16
242     <211> LENGTH: 33
243     <212> TYPE: DNA
244     <213> ORGANISM: Artificial Sequence
```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/104,340**

Input Set: **I104340.RAW**

Line	?	Error/Warning	Original Text
266	W	"N" or "Xaa" used: Feature required	ccratgggna ccagccaytc